

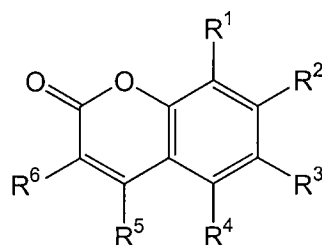
Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1-83 (canceled)

84 (previously presented): A material having a fluorogenic moiety linked to a solid support, said material having the structure:



wherein:

R¹, R³, R⁴ and R⁶ are each H;

R² is -NHR¹⁵; and

R⁵ is -R¹⁴-SS,

wherein:

R¹⁴ is -CH₂C(O)NH-;

R¹⁵ is a member selected from the group consisting of amine protecting groups, -C(O)-AA and -C(O)-P:

wherein:

P is a peptide sequence;

AA is an amino acid residue; and

SS is a solid support.

85 (previously presented): The material in accordance with claim **84**, wherein R¹⁵ is an amine protecting group.

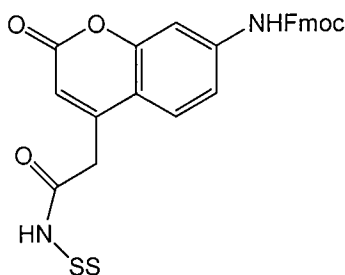
1 **86** (previously presented): The material in accordance with claim **85**, wherein
2 said amine protecting group is 9-fluorenylmethoxycarbonyl (Fmoc).

1 **87** (previously presented): The material in accordance with claim **84**, wherein
2 R^{15} is $-C(O)-AA$, wherein AA is an amino acid residue.

1 **88** (previously presented): The material in accordance with claim **84**, wherein
2 R^{15} is $-C(O)-P$, wherein P is a peptide sequence.

1 **89** (previously presented): The material in accordance with claim **84**, wherein
2 the solid support is a Rink resin.

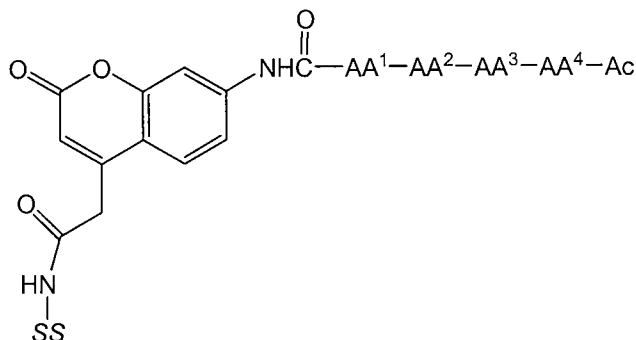
1 **90** (previously presented): A material having a fluorogenic moiety linked to a
2 solid support, said material having the structure:



3
4 wherein:

5 SS is a solid support, wherein said the support is a Rink resin.

1 **91** (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1,
2 P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides
3 having the structure:



wherein:

SS is a solid support, and

wherein:

for sub-library P1, each AA¹ is a different amino acid of the 20 amino acids, and each of AA²-AA⁴ is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA² is a different amino acid of the 20 amino acids, and each of AA¹, AA³ and AA⁴ is an isokinetic mixture of 20 amino acids;

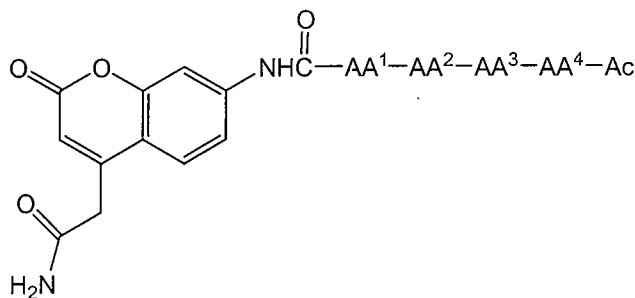
for sub-library P3, each of AA³ is a different amino acid of the 20 amino acids, and each of AA¹, AA² and AA⁴ is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA⁴ is a different amino acid of the 20 amino acids, and each of AA¹, AA² and AA³ is an isokinetic mixture of 20 amino acids.

92 (withdrawn): The library in accordance with claim **91**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

93 (withdrawn): The library in accordance with claim **91**, wherein the solid support is a Rink resin.

94 (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides having the structure:



wherein:

for sub-library P1, each AA¹ is a different amino acid of the 20 amino acids, and each of AA²-AA⁴ is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA² is a different amino acid of the 20 amino acids, and each of AA¹, AA³ and AA⁴ is an isokinetic mixture of 20 amino acids;

for sub-library P3, each of AA³ is a different amino acid of the 20 amino acids, and each of AA¹, AA² and AA⁴ is an isokinetic mixture of 20 amino acids; and

for sub-library P4, each of AA⁴ is a different amino acid of the 20 amino acids, and each of AA¹, AA² and AA³ is an isokinetic mixture of 20 amino acids.

95 (withdrawn): The library in accordance with claim **94**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

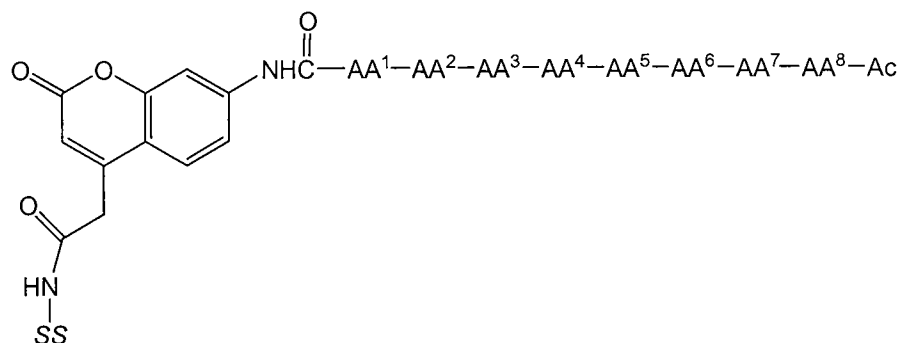
96 (withdrawn): A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

- (a) contacting said protease with a library of peptides according to claim **91** or claim **94** in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;
- (b) detecting said fluorescent moiety;
- (c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

1 **97** (withdrawn): The method according to claim **96**, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **98** (withdrawn): The method according to claim **97**, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.

1 **99** (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1,
2 P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides
3 having the structure:



4 wherein:

5 SS is a solid support, and

6 wherein:

7 for each sub-library P1, P2, P3 and P4, AA¹, AA², AA³ and AA⁴ in each of the
8 hexapeptides are the same amino acid residues;

9 for sub-library P1, each of AA⁵ is a different amino acid of the 20 amino acids,
10 and each of AA⁶, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

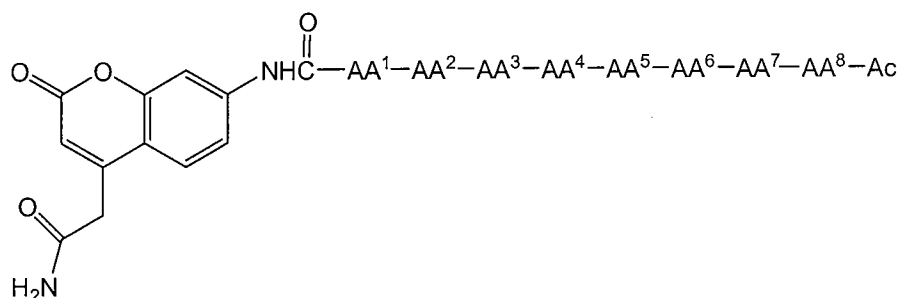
11 for sub-library P2, each of AA⁶ is a different amino acid of the 20 amino acids,
12 and each of AA⁵, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;
13

for sub-library P3, each of AA⁷ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁸ is an isokinetic mixture of 20 amino acids; and
for sub-library P4, each of AA⁸ is a different amino acid of the 20 amino acids,
and each of AA⁵, AA⁶ and AA⁷ is an isokinetic mixture of 20 amino acids.

100 (withdrawn): The library in accordance with claim **99**, wherein the 20 amino acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

101 (withdrawn): The library in accordance with claim **99**, wherein the solid support is a Rink resin.

102 (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1, P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides having the structure:



wherein:

for each sub-library P1, P2, P3 and P4, AA¹, AA², AA³ and AA⁴ in each of the hexapeptides are the same amino acid residues;

for sub-library P1, each of AA⁵ is a different amino acid of the 20 amino acids, and each of AA⁶, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

for sub-library P2, each of AA⁶ is a different amino acid of the 20 amino acids, and each of AA⁵, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

12 for sub-library P3, each of AA⁷ is a different amino acid of the 20 amino acids,
13 and each of AA⁵, AA⁶ and AA⁸ is an isokinetic mixture of 20 amino acids; and
14 for sub-library P4, each of AA⁸ is a different amino acid of the 20 amino acids,
15 and each of AA⁵, AA⁶ and AA⁷ is an isokinetic mixture of 20 amino acids.

1 **103** (withdrawn): The library in accordance with claim **102**, wherein the 20
2 amino acids are the 20 naturally occurring amino acids excluding cysteine and including
3 norleucine.

1 **104** (withdrawn): A method of determining a peptide sequence specificity profile
2 of an enzymatically active protease, said method comprising:

3 (a) contacting said protease with a library of peptides according to claim **99** or
4 claim **102** in such a manner whereby the fluorogenic moiety is released
5 from the peptide sequence, thereby forming a fluorescent moiety;

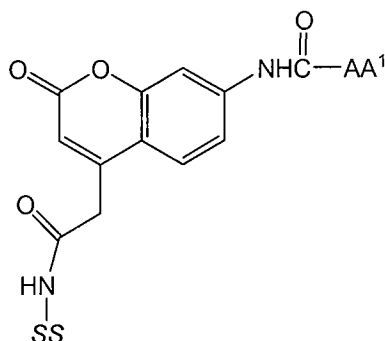
6 (b) detecting said fluorescent moiety;

7 (c) determining the sequence of said peptide sequence, thereby determining said
8 peptide sequence specificity profile of said protease.

1 **105** (withdrawn): The method according to claim **104**, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **106** (withdrawn): The method according to claim **105**, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.

1 **107** (withdrawn): A library of twenty fluorogenic amino acid amides having the
2 structure:



wherein:

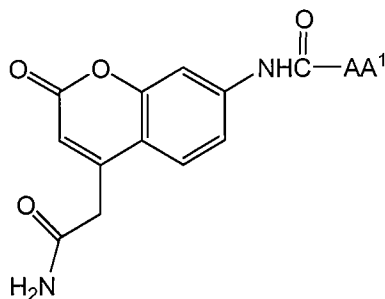
SS is a solid support, and

each AA¹ for the twenty fluorogenic amino acid amides is a different amino acid residue.

108 (withdrawn): The library in accordance with claim **107**, wherein the amino acid residues are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

109 (withdrawn): The library in accordance with claim **108**, wherein the solid support is a Rink resin.

110 (withdrawn): A library of twenty fluorogenic amino acids having the structure:



wherein:

each AA¹ for the twenty fluorogenic amino acids is a different amino acid residue

1 **111** (withdrawn): The library in accordance with claim **110**, wherein the amino
2 acid residues are the 20 naturally occurring amino acids excluding cysteine and including
3 norleucine..

1 **112** (withdrawn): A method of determining an amino acid specificity profile of
2 an enzymatically active protease, said method comprising:

3 (a) contacting said protease with a library of amino acids according to claim **108**
4 or claim **110** in such a manner whereby the fluorogenic moiety is released
5 from the amino acid, thereby forming a fluorescent moiety;

6 (b) detecting said fluorescent moiety;

7 (c) determining the identity of the amino acid, thereby determining said amino
8 acid specificity profile of said protease.

1 **113** (withdrawn): The method according to claim **112**, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **114** (withdrawn): The method according to claim **113**, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.